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Val Ala	Trp Tyr 35	Gln Gl	n Lys	Pro 40	Gly	Lys	Ala	Pro	Lys 45	Leu	Leu	Ile
Tyr Ser 50	Ala Ser	Phe Le	u Glu 55	Ser	Gly	Val	Pro	Ser 60	Arg	Phe	Ser	Gly
Ser Arg	g Ser Gly	Thr As		Thr	Leu	Thr	Ile 75	Ser	Ser	Leu	Gln	Pro 80
Glu Asp	Phe Ala	Thr Ty 85	r Tyr	Cys	Gln	Gln 90	His	Tyr	Thr	Thr	Pro 95	Pro

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35 40 45

Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Ala Asp Ser Val 50 60

Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
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<223> single chain Fv with zipper domain

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cctgtgctgc ctcgggtcgt actggttcta cttatgatat gggctggttt cqtcaqqctc
                                                                     120
cgggtaaaga acgtgaatcg gttgccgcca ttaactggga ttcggctcgt acttactatg
                                                                     180
cttcgtccgt ccgtggtcgt tttactattt cacgtgataa tgccaaaaaa actgtctatt
                                                                     240
tgcagatgaa ttcattgaaa ccagaagata ctgccgtcta tacttgtggt gctggtgaag
                                                                     300
geggtaettg ggattettgg ggteagggta ceeaggteae tgteteetet geeggtggta
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Gly Ser Thr Tyr
Asp Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Ser Val
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Arg Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Thr Val Tyr

Ala Ala Ile Asn Trp Asp Ser Ala Arg Thr Tyr Tyr Ala Ser Ser Val

55

50

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Thr Cys
85 90 95

Gly Ala Gly Glu Gly Gly Thr Trp Asp Ser Trp Gly Gln Gly Thr Gln
100 105 110

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Lys

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<400> 137

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<210> 138

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Arg Ile Xaa Cys

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Xaa Xaa Xaa Xaa Xaa 20

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<220>
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<220>
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Xaa Xaa Xaa Xaa Xaa Xaa Xaa
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Xaa
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Xaa
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                                                                     60
nnsnnsnnsn nsnnstgggg tcagggt
                                                                     87
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kccksggytr ctksgtgggg tcagggt
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rctsstgyts makcctgggg tcagggt
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      (74)...(74)
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                                                                     60
                                                                      87
kytgstsytg ytgsttgggg tcagggt
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                                                                      60
                                                                      86
gmarygscas ytgcgtgggg tcaggg
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Trp
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Ser
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Ala
<210> 168
<211> 17
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Val Leu Glu Leu Arg Ser Ser Gly Gly Asn Ala Arg Trp Met Ser Leu
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Tyr
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                                   10
Tyr
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<211> 17
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                                   10
Phe
<210> 171
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10

Ala

<210> 172

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Ser
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               5
                                   10
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Ala Xaa Xaa Xaa Xaa Xaa Trp Xaa Tyr Ala Met Asp Tyr
               5
                                   10
<210> 176
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<400> 176
Ala Xaa Xaa Xaa Xaa Xaa Xaa Trp Tyr Ala Met Asp Tyr
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           20
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Arg Ile Xaa Cys Xaa Xaa Xaa Xaa Xaa Cys Trp Val Xaa Xaa

1 5 10 15